

Amendment to the Claims

The following listing of claims will replace all prior versions and listing of claims in the application.

1 – 4. (Canceled)

5. (Currently amended) A nucleic acid encoding a variant ~~as claimed in claim 41~~ of the PapM polypeptide of bacteria of the Streptomyces genus comprising SEQ ID NO:1, selected from the group consisting of
- a polypeptide comprising the sequence of a wild-type PapM polypeptide of S. pristinaespiralis modified by the replacement of residue Gly 249,
- a polypeptide comprising the sequence of a wild-type PapM polypeptide of S. pristinaespiralis modified by the replacement of residue Thr 192,
- a polypeptide comprising the sequence of a wild-type PapM polypeptide of S. pristinaespiralis modified by the replacement of residues Gly 249 and Thr 192,
- and a polypeptide of a bacteria of the Streptomyces genus which is homologous to the wild-type PapM polypeptide of S. pristinaespiralis and is modified by the replacement of one or more of the residues equivalent to Gly 249 and Thr 192 in the wild-type PapM polypeptide of S. pristinaespiralis;
- wherein the variant of the PapM polypeptide
- catalyzes at least one of the methylation of PAPA to MMPAPA and the methylation of MMPAPA to DMPAPA and
- exhibits an efficiency of methylation, as defined by the ratio K_{cat}/K_m , which differs from the efficiency of methylation of the wild-type PapM polypeptide of S. pristinaespiralis for at least one of the methylations of PAPA or MMPAPA.

6. (Currently amended) ~~The A~~ nucleic acid as ~~claimed in claim 5~~, comprising SEQ ID NO. 1 modified by mutation for the replacement of at least one of Gly 249 or Thr 192 and optionally modified by the replacement of at least one codon with an alternate codon encoding the same amino acid due to the degeneracy of the genetic code.
7. (Original) The nucleic acid as claimed in claim 6, which comprises at least one missense mutation upstream of the NPPY motif located at positions 193 to 196.
8. (Original) The nucleic acid as claimed in claim 7, wherein the missense mutation leads to a non-conservative amino acid change.
9. (Previously presented) The nucleic acid as claimed in claim 8, which comprises the substitution of a cytosine at position 658 with a thymine (C658T).
10. (Previously presented) The nucleic acid as claimed in claim 6, which comprises the substitution of a guanine at position 828 with an adenine (G828A).
11. (Previously presented) The nucleic acid as claimed in claim 8, which comprises the substitution of a guanine at position 828 with an adenine (G828A), and the substitution of a cytosine at position 658 with a thymine (C658T).
12. (Canceled)
13. (Previously presented) An expression vector which replicates autonomously and/or which integrates in a bacterial strain, comprising a nucleic acid as claimed in claim 5.
14. (Canceled)
15. (Currently amended) A host cell containing a nucleic acid as claimed in claim 5 or claim 6.
16. (Previously presented) The host cell as claimed in claim 15, selected from the group consisting of *E. coli*, *S. pristinaespiralis*, *Streptomyces olivaceus* ATCC12019, *Streptomyces ostreogriseus* ATCC27455, *Streptomyces mitakaensis* ATCC15297, *Streptomyces loïdensis* ATCC11415, *Streptomyces graminofaciens* and *Streptomyces diastaticus*, each containing a nucleic acid as claimed in claim 5.

17 - 42. (Canceled)